PROGRAMME & ABSTRACT

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DIVERSITY OF MARINE MACROALGAE IN SELECTED SABAH MARINE PARKS

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Four marine parks in Sabah, namely Pulau Sapi, Pulau Memutik, Pulau Sulug and Pulau Manukan has been studied for its marine macro algae diversity. A total of 15 families and 42 species from three divisions (Chlorophyta, Rhodophyta and Pheophyta) have been identified. The highest number of species was collected in Pulau Sapi (34), Pulau Manukan (32), Pulau Sulug (25), and Pulau Memutik (22). Division Chorophyta scored the highest number of species recorded with 18 species, followed by Pheophyta with 15 species and lastly Rhophyta with 13 species. These studies have revealed unexpected discovery of many new records and pattern of species dominance. Pulau Manukan recorded the highest number of new records with 27 species, Pulau Sapi and Pulau Memutik with 18 and 8 respectively. Pulau Sulug does not have any new record. The species dominance pattern in the four islands showed a positive correlation with the number of species per division. Islands that have the high number of species from division Chlorophyta have recorded *Caulerpa* and *Halimeda* as the most dominan genus. Where as when high number species recorded for Pheophyta, the genus *Turbinaria* and *Sargassum* was seen as co dominant with *Caulerpa* and *Halimeda*. Conclusively, these marine parks are rich in species diversity with division Chlorophyta leading the list, followed by Pheophyta and lastly Rhodophyta.

MORPHOMETRIC INVESTIGATION OF FIVE LABEOIN SPECIES BASED ON THE TRUSS NETWORK

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A morphometric investigation was conducted on five species within the Labeoin group, *Labiobarbus festivus, L. leptocheilus, Morulis chrysophekadion, Osteochillus hasselti* and *O. vittatus*. The twenty seven characters chosen were measured based on the truss network concept. Four of the species were sampled from various locations in Peninsular Malaysia while the fifth, *Morulis chrysophekadion* was from Lake Tonle Sap in Cambodia. The results were analysed using univariate analysis of variance (ANOVA) and multivariate discriminant function analysis (DFA). The scatter plot obtained from the latter analysis successfully discriminated each species clearly. This study shows the potential of these characters in clarifying less well-defined species within this group.

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INTRODUCTION

The fundamental aspect of truss network is to describe the body form in order to sought contrasts between the classes of objects, be they the species, population or individual shapes as a guide to discrimination (Winfield and Nelson, 1991). Proposed by Strauss and Bookstein (1982), this method has several advantages over the conventional character data sets; 1. it removes bias of distance measurements that generally tend to be aligned to only a few axes resulting in an uneven coverage of form 2. it also reduces bias to the covariance structure of the data when long distances are measured in the traditional method compared to short distances as in the truss method.

Leong (2003) did a comprehensive study of this group on five species in the genus *Labiobarbus* found in Peninsular Malaysia based on morphological and RAPD techniques. This paper forms part of a larger study of the Labeoin group in Malaysia and Cambodia. The taxonomic status of many species within the genus *Labiobarbus* and Labeoin group has been well-defined (Roberts, 1993; Kottelat & Whitten, 1996). However, there still remains some controversy over several presumed species. Although the five species investigated in this study are clearly characterised by conventional means, the findings from this approach offers an alternative to investigate other less well defined species within this group.

MATERIALS & METHODS

Sample collection

The samples as summarized in Table 1 were either caught or purchased from fishermen. Each individual was identified using the taxonomic keys described by Roberts (1993) and Kottelat (1996).

Table 1 : Sample profiles used in truss analysis.

Species	Sites	N
Labiobarbus festivus	Tasek Bera, Pahang,	34
Labiobarbus leptocheilus	Tasek Chini, Pahang	20
Morulis chrysophekadion	Tonle Sap Lake, Cambodia	20
Osteochillus hasselti	Tasek Chini, Pahang	29
Osteochillus vittatus	Ahning Dam, Kedah	4
	Tasek Bera, Pahang	1

Truss Network Measurements

Each sample was laid out on a polystyrene board and pinned. Twenty seven linear measurements, labelled A1 to E6 (Figure 1) including standard length were taken between twelve homologous points; (1) anterior tip of the snout; (2) posterior point of the neuracranium; (3) origin of the dorsal fin; (4) origin of the 5th ray of the dorsal fin; (5) posterior end of the dorsal fin; (6) dorsal origin of the caudal fin; (7) ventral origin of the dorsal fin; (8) insertion of the anal fin; (9) origin of the anal fin; (10) insertion of the pelvic fin; (11) origin of the pelvic fin and (12) origin of the sub-operculum. Measurements were conducted on the left side of each specimen by using a pair of digital calipers. In order to standardise the different sizes of specimen due to differing allometric growth, a transformation formula (Palma & Andrade, 2001) was applied to the raw data.

$$M_{trans} = \log M - \beta(\log SL - \log Sl_{mean})$$

M_{trans} is the transformed measurement, M the original measurement, β the within group slope regressions of the log M vs. log SL, SL the standard length of the fish and SL_{mean} the individual mean for each species of the standard length. Univariate analysis was conducted to determine characters that were significantly different for the multivariate analysis. The multivariate analysis, Discriminant Function Analysis (DFA) was then conducted on the chosen characters. All analysis was performed based on the transformed data using SPSS software version 11.5.

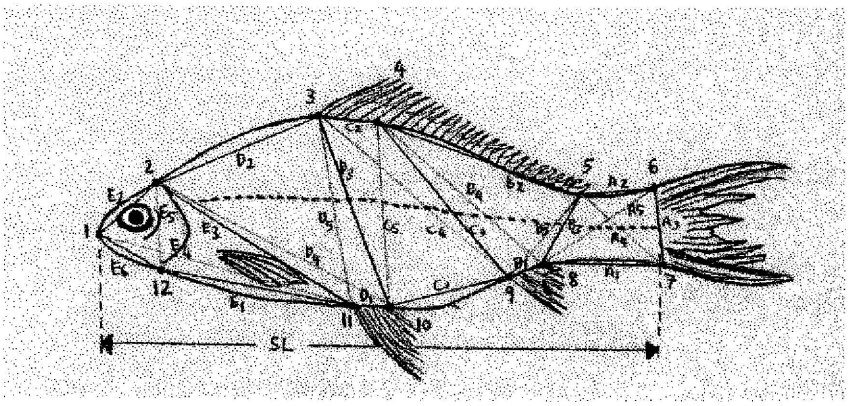


Figure 1: Truss network formed by lines joining 12 homologous landmarks.

RESULTS

Results of ANOVA showed that all characters were significant at 95% confidence level (data not shown) and therefore all variables were retained in the multivariate analysis. In the DFA analysis (Table 3), components 1 and 2 with eigenvalues of 276.7 and 100.7 explained 69.7 % and 25.4% of the variance among species. Based on the standardized canonical discriminant function coefficient (Table 2), nine characteristics, A4, B2, C4, C5, D2, D5, E2, E3 and E4 have been identified as the most important variables in discriminating the Labeoin species.

The scatter plot completely discriminated all individuals to their correct taxon based on their initial identification by traditional characters.

Table 2 : Standardized Canonical Discriminant Function Coefficients for 27 characters.

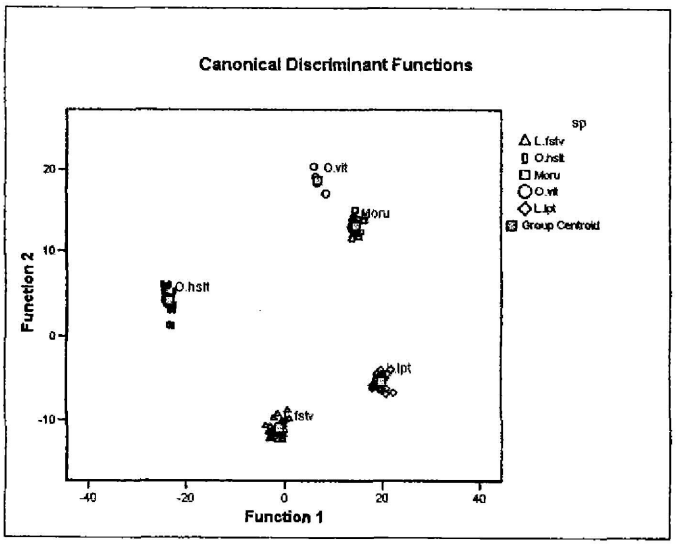
	Function			
	1	2	3	4
A1	.168	-.095	-.483	-.608
A2	.103	.226	.080	-.006
A3	.078	.307	.426	.273
A4	.529	.281	.015	.421
A5	.268	-.200	.220	.084
B1	.141	.421	.055	.413
B2	.423	-.614	.848	.935
B3	-.049	.173	.023	.164
B4	.271	.026	-.959	-.745
B5	-.133	.322	-.157	.302
C1	.262	.156	-.212	.170
C2	.117	.219	-.601	.266
C3	-.111	-.089	.298	-.064
C4	.360	-.141	-.323	.033
C5	-.334	-.252	.184	-.755
D1	-.150	-.161	-.184	-.415
D2	.398	-.001	.276	-.125
D3	-.013	-.172	-.032	.103
D4	-.105	-.035	-.110	.148
D5	-.525	-.169	.578	.323
E1	.174	-.053	.014	.103
E2	.375	-.082	.669	-.370
E3	.547	.148	-.048	.241
E4	.663	-.046	-.315	-.295
E5	-.274	.473	.092	.484
E6	-.024	.204	.489	-.352
SL	.068	-.002	-.008	.005

Table 3 : Eigenvalues, percentage of variance, cumulative percentage and canonical correlation of function 1-4.

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	276.709(a)	69.7	69.7	.998
2	100.723(a)	25.4	95.1	.995
3	12.963(a)	3.3	98.4	.964
4	6.395(a)	1.6	100.0	.930

a First 4 canonical discriminant functions were used in the analysis.

Figure 2 : Scatter plots generated via DFA for Function 2 vs. Function 1.



DISCUSSION

This study has shown that the truss network is an effective method in discriminating among five species of the Labeoin group. Due to its ease and low cost involved it will be a useful technique in our multi-approach investigation of the systematics and phylogenetics of the Labeoin group. Other markers to be included in future study is the 16S rRNA mitochondrial DNA. The findings will contribute towards the taxonomic clarification of this group.

ACKNOWLEDGEMENTS

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